



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ruddy, David A.
Wolff, Roger K.
- (ii) TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
HEMOCHROMATOSIS GENE
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pennie & Edmonds, LLP
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10036-2811
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/852,495
(B) FILING DATE: 07-MAY-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Poissant, Brian M
(B) REGISTRATION NUMBER: 28,462
(C) REFERENCE/DOCKET NUMBER: 8907-0057-999
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-493-4935
(B) TELEFAX: 650-493-5556
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235033 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CACACACACA CACACACACA CACACACACA CACACAAATG AGGTATATAA AGGGTCTCCT	60
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CTATTTT TAGA TAGCCTTGTC TGAAACAGAG CTGGGACCTG ATGAGTGAAA ATGAGCTCAC	180
CAGAAGAAAA ATCAAACAGG CATTTTCAGAG ATTGAGGCCA AGAAGTTAAA TGTCTTAAAT	240
GGGCAGAGCT TAGCTGCTTG ATGTGAAAAG AGACCAGCGT GGCTGGAACA GCAAAGGAGA	300
ACAGCAGAAG AGGTGAACAG AGGCCAGAGA TGGTCACTGA GTGGGCCCTT AAGTCATGGT	360
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TACTTTGGAT TTGTAGAGAT GAAGGAAATG TAGCAAGTGA CACTCTTAGA ATGTTGATTT	480
GAGTAAATGG TAGTGTCAGT TATTGAACTG GGGAGAACTG GAAGGGATAA CAGGCTTAAG	540
GAGCACGTTT ATTCCTGTGT CTTGGAAGTG TTTAGGGTGA AAGACCTATT AGAGTTCTAA	600
ATGGAGATGT CAAGTGAAAA TGTGGCTACA CACATTTGCA TTTCAGAAAA AAGGTCAGGC	660
TGGAGATGTA AAATTGGAAG TTTACTGCAT ATAGATAGTC TTTGGAACCG TAGTATTGAT	720
GAAGCCATTA ATGAGACAGA ACAAAGACTA GGGACCAGAG CCAAGCTCCA AGTTTCTAAA	780
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GACTAAGTTT TGGTACCCAG GCGTGGGATG CTGCAACAAC AAATACCTAA ACATGGGGAA	1140
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GGCTCACGCC TGTAATCTCA GCACTTTGGG AGGCTGAGGG CACAGATCAC GAGGTCGGGA	1440
GTTTGAGACC AGCCTGGCCA ATATGGCGAA ACCCTGTCTC TACTAAAAAT ACAAAAATTA	1500
GCTGGGCATG GTGATGTGCT TCTGTGGTCC CAGCTACTCG GGAGGCTGAG GCTGAAGAAT	1560

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GGACATTAAA	GTCAACTCTT	GTGAGGTCTC	AGATGAAAAT	GAGGGACAGG	TTATTGGAAA	1740
CTGTAGAAAT	CACTGTTCTT	GTTACAATGT	GTCAAGAACT	TGGCTGAATT	ACGCTGTAGT	1800
GTTTACTGGA	AAGAACTTAT	AAGCAGTAAA	ACTGGATATT	TACCAGAAGA	GATGTCTAAG	1860
CAAAGTATTG	AAGGTGTGAT	TTAGGTCCTC	CTTACTGCTT	AAAGTGAAAT	GTGAGAGGAA	1920
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ACAATGTTTT	CTTTTTCTTT	TTTTTCTTG	GTTTTATTTT	TATTTTTATG	TTTTTTGAGA	2100
CAGGGTCTGG	CTATGTCATC	CAGGCTGGAG	TGCAGTGGCA	CAATCTCAGT	TCAGTGCAAC	2160
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AGATGACACT	TTGAACTTTA	GAATTGATGC	TAGAATGAGT	TAAGACTTTC	AGGGGGCTGT	3540
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GAGCTCTCTC	TCCACGCAGG	CACCAAGGAA	ACACCATACA	AACACACAGT	GAGATGGCAG	4140
CCATCTGTTA	GCCAGGAACA	GATTCTCACC	ATAAACTATG	TTGGCACCTT	GATCTTAAAC	4200
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GCTAAGACAA	TGAAGGATGT	GGTAAACTT	TACGTCCCCA	CCACATACCA	AAGAGGCTGG	4380
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CATCCAATGA	AGTTCTGACA	TTTCTTCAAC	ATGAGTACAG	TAATTCAATG	CCAGAGAATT	4560
CATTTTATTT	TGAAATCTAC	ATGCCATATT	CCAATTTCTG	TTGAAGATGC	AATGGTTATA	4620
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TGATTCTCTT	GCCTCAGCCT	CCCAGTAGTC	TGGGACTACA	GGCGTGCACT	AGCATGCCCA	6180
GCTAATTTTT	GTATTTTTTA	GTAGAGATGG	GGTTGGTTTT	TTTTTGAGAC	GGAGTTTCAC	6240
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GGTGAACACC	GCCACACCTG	ACTAATTTGT	GTAGTTTTAT	TAGAGATGGG	GTTTCGCCAT	6420
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TCACCACAAT	AAGTCAGTTG	CACCAAGTCT	TGTAGCTCTT	TACTGAGCCA	TGTTTTACAG	6960
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TACCTTTCCT	CCTTCCCTTA	AATTCTTCAG	AGGTTAGAAA	GCCATTAGTA	ACATTCTGGT	7140
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AATCTCTTAA	GGAGGTGTGG	TTATAGAATA	GTCAGCTGTT	ATAAGTACTG	TTTTCTGGC	7260
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CAGGCTCAAG	CGACTCTCCT	GCGTCAGCTT	CAAGAGTAGC	TGGGATTACA	AGGTATGTGC	8760
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CATAAAAGCC	CTATAAGTAG	CAGAAATCCG	CTCTTTACTT	TCGACACATT	TCTGGTGTTT	10320
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TTTACATAGC	GGACCGGAGT	GGGAACCTGG	GCAGTAACTG	CCTAAGGAAG	GACTCCCCCT	11220
CTGTTTTTCGT	GGCGCACACC	TTCGTAGTAT	ACTGAAGGGT	GTGTCTCCTG	GGTTTCCAAC	11280
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ACTGGTTTAT	TCAAGATTCA	AATCAAATCA	AATTTTGCTT	GAATCCCAGT	GCTCAGTCAG	11460
CCATAAATGG	TGTGTTGCCT	GATTGAAACT	TAAAATCTCC	GTAGGGGGCT	TGTAACATGC	11520
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GCCTTCGAAC	ACTGAACTGA	AGGCCAGTAA	GGACTAGGCG	CTGGGTGGGG	GAGAATGAAG	11640

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GGTCTTTTCC	AGGTAAAGAT	TTTAAGATGA	AGGGTTAGAC	GTAGTCTACC	TATCTTTTTA	11820
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CCTGGGAAAT	AACTAAGGC	CTGTCTTTGG	TGCCAGACAA	GGCCTTATAC	TTGAACACTG	12060
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CAAATGTTAT	TTAATAAAAC	AATGGGGTCA	CCCTTAGTCT	AAAAGATGTT	TCACTTTTCA	76260
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ATGCCTAGCC	ATGTCTCTCT	CCTTATATAT	AATAAGAAAA	CAGACACACT	GAGGCATCCT	225540
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GCCTTTAGGT	ATTTTCACAC	TTGCTCTGTT	ACGTAAATGT	ATGTGTGTGT	GTGTGTGTGT	235020
GTGTGTGTGT	GTG					235033

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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AACAAAGGAA	GGTTGTGCGAC	TTTTTGAATT	CTATAGAACA	GGATCATAGA	GCTACCTGGC	2580
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GATCACTAGG	GCTGACTCTT	TTTTGTTTTT	TCTTGAGGCA	GTCTCACTGT	CACCCAGGCT	2700
GTAGGGCAAT	GGTGTGATCT	CAGCTCACTG	CAATCTCCAC	CTCCCAGGTT	CAAGGGATTC	2760
TCTTGCCTTA	GACTCCCAAG	TAGCTGGGAT	TACAGGCTCT	AAATCTGTAC	CCTCCCGAGT	2820
AGCGCTCCTG	CCACCACTTG	CCCAGCTAAT	TTTTGTATTT	TTAGTAGAGA	TGGGGTTTCA	2880
CTATGTTGGC	CAGGCTAGTT	TGGAACCTCT	GACCTCCAGT	GATCCATTCT	CATTGGCCTC	2940
CCAAAGTGCT	GGGATTACAG	GCAGGAGCCG	CCAGGGCTGC	CACTTTGATG	TCAGACTCAG	3000

AGAGTACAGA	TGGGATAGGG	TGGGGGTGGG	AACATGTAGT	CAAGGCTGAC	TCTACCTGTT	3060
TCAAAGATGC	CCTGCAGAAC	TGTGTGGGAG	TCTCTCACAG	ATGGCTGCCT	GGGTGGGACC	3120
CCACCAAAC	GAAAGACCGA	GACTTCAGGC	AGGGCAGATG	GAGTAGGCCA	ACTACAGAGC	3180
CAGAGGTGAC	ACTGAGACAC	CACTGGGCCT	GGAAATCAGG	GCATCAAGCC	AAAGAGGGTT	3240
TTTCTTAAGA	CCTAACAGAA	TTTGCCTTGC	CAGGTTTTTG	ACTTGATTAG	GACACATTAC	3300
ACCTTCCTTC	TTTCCTATTT	CTCCATTTTC	TAATGGGAAT	GTCTATTATG	CCTGTTTCAC	3360
CATTGTACCT	TAGAAGCATG	TAACATTTCT	GGTTTCACAC	GTTCAAAGCT	GGAAAGGAAT	3420
TTTGTCTCTG	GATGAATCAC	ACATTGAGCC	TCACCCGTAA	CCTGATTTAG	ATGATTTTTT	3480
AGATGACACT	TTGAACTTTA	GAATTGATGC	TAGAATGAGT	TAAGACTTTC	AGGGGGCTGT	3540
TGGGATGGAA	TAATTTTTTT	TTTTTTTTTG	AGACGGAGTC	TAGCTCTGTC	GCCCAGGCTG	3600
GAGTGCAGTG	GCACCATCTT	GGCTCACTGC	AAGCTCTGCC	TCCCGGGTTT	ATGCCATTCT	3660
CATGTCTCAG	CCTCCAGAGT	AGCTGGGACT	ACAGGCGCCC	GCCACCACGC	CTGGCTAATT	3720
TTTTTTTTTAT	TTTAGTAGAG	ATGGGGTTTC	ACCGTGTTAG	CCAGAACGGT	CTCGATCTCT	3780
TGACCTTCTG	ATCCGCCTGC	CTTGGCTTCC	CAAAGTGCTG	GGATTACAGG	TGTGAGCCAC	3840
CATGCCCCGC	TGGGATGGAA	TAAATTTATC	TTGTATGGGA	GAAGGACATA	CATTTTGGCA	3900
GGTCAAGGAC	AGAATGTTAT	GGACTAAACT	GTGTCCCCCA	AAATTCATTT	ATTAAAACCC	3960
TAAACCCCAG	TGTGACTGCA	TTTGGACATA	GAGCCTTTAG	GGGGTACATA	AAACTAAAGA	4020
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GAGCTCTCTC	TCCACGCAGG	CACCAAGGAA	ACACCATACA	AACACACAGT	GAGATGGCAG	4140
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GCTAAGACAA	TGAAGGATGT	GGTAAACTT	TACGTCCCAA	CCACATACCA	AAGAGGCTGG	4380
AATTTAGCAT	GCTTTCTTCT	TTCAACTGTA	GGCAATGTGC	ACAAGTTCTA	AATCCTAAGA	4440
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CATTTTATTT	TGAAATCTAC	ATGCCATATT	CCAATTTCTG	TTGAAGATGC	AATGGTTATA	4620
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TGCCTGTAGT	CCCAGTTACT	AGGGAGGCTG	AGGTAGAATT	GCTTGAACCT	GGGAGCAGGA	4860
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ATTTGCTCAT	CTCCAATATG	CACGGGAAAT	TCTCAAATTG	CTAATAATCT	TGTAACACAC	5160
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TTCAAGTGAT	TCTTCTGCCT	CAGTCTCCTG	AGTAGCTGGG	ACTACAGGCG	CCTACAGGTG	6360

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GCCAGGCTGG	TCTCAAACCTC	CTGACCTCAG	GTGATCTACC	CACCTCAGCC	TCCCCAAGTG	6480
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 TTTGAGATCA GCCTGGGCAA CATAGTGAGA CCCTGCCTCT GTAGAAATAA ACAAAAATTA 234540
 GCTGGATATG GTGGTGCATG CTTGTACTCC TAGCTACTTG GGAGGTTGAG GCAGGAGGAT 234600
 CCTTTGAGTC CAGGAGTTTG AGGCTGCAGT GAGCTATAAT CACCCACTGC ACTATAGCAT 234660
 GGGCAATAAG GTGAGAACTT GTCTCAAAAA AAAAAGGGGG GGGGGAAACA AATAAATAAA 234720
 TATAACAAA ACTTTTGTTC CAAAATATGT AATATTTAGC ACTAAAGAAT TCTGAATTGT 234780
 AGAGCTAAAA AGTACTTAAA AGTTAATAAC TATTGTCTCC TTTAAAAGAA TTGTTATCAA 234840

AGTATAATTT TTATCCAGAA AATCATCCAT ATCAGCAAGC TAAACTTTCT CAAAATGACA 234900
 TATCCATGTA ATTAGCTCCC AGGTAATTAG CAGGCAGCCT CTACTCAGGT TGAGTATTCC 234960
 TAATCTAAAA ATTGGAAATT CAAAATGCTC CAAAATCTGC AACTTTTTGA ATGCTAACAT 235020
 GATTCTCAAA GGAGTGCTCA TGGAGTATTT CAGATTTTGG ATTTTGGAT TTGAGATACT 235080
 CAGTATAATG CAAACATTCC AAATCTGAAA AAATCTGAAA TACTTCTGGT TCTAAGCATA 235140
 AGGGATACTC AACGTGTGTT AGCTAATTAG ACCCTTCATG GTCTCTTCTA GACCTCAGCT 235200
 TCTTCAAGGT AACCTCTATC CTCACTTCTA ATAGCATGAA CTTTTCTGTT TTAGAATAAT 235260
 TTGGATTTTC AGGAAAGTTG CAAAGATAGT ACAAAGACAG TACAGGAGAG TTCCCATATA 235320
 TCTTTCACCT AGCTTTCCCC CATTGTTAGG ATTTTACATT ATTATGATAC ATTTGTCAAA 235380
 TATAAGCAAC TCACATTGAT ACATGAAACT CTATTAACCA AACCCTAGAC TTTATGTGGA 235440
 TTTCACCACT GTTCCACTA ATGTTTTCTT TCTGTTCCAA GGTCCAATCT GGAATACCAC 235500
 ACTGCATTTT CTTGTCATAT CTCCCTAGTC TTTTTTTGTC TGTGACAATG TCTCAGTCTT 235560
 TTCTTGCTTT TCATGACCTT AACAGTCCTG AAGATCATTT GCTTTTTTTT CATAATTACA 235620
 CCGGAGTTAT AGATTTTTTG AAATAATACC ACAAGGGCAA AGGGCCCTTC TTGTCACATC 235680
 ATTTTAGGGA GAACATGATA TCCACATGAC ATCACTGATA TTAACCTTCA TCATGTGGTT 235740
 TAGGTAATGT TTCAGGTTTC TCTACTGCAA AGTGATTTTT TTCCCTTAAT TTAGCCCACC 235800
 TGAACCTATC AATTTTGTTT TCTTCCATGA CTAATACTTT TGTTATTATA GCTAAACTT 235860
 CATTGGGGCC AAATCTTAGA TCATGTAAAT TTTCTTCTAT ATTTTATTCT AAAAGCTTGT 235920
 AATGTTTGAT ACATTCTAAA AGATGTAATG TTTGATACAT TACATCTAGT CCTTTGATTT 235980
 ATTTTLAGTT ACTTTTGAT AAGGTGTGAG AGATGTCTCC AGTTTCACTT TATTAACACA 236040
 TTGTGGTGTT CCAGTACTAT TTGTTGCTAA GACTATCTTT TTTCCATTGA TTACCTTTGC 236100
 CTTAGTTGGC AATATTTTTG TTGGTTTATT TCTAGACTGT TTATCTCATT CCACTGATTT 236160
 GTGTCTATCT TTTTGACAAA ACTGTTGATT ACAGTAAGCT TTGAAATAGT TCATTTTTTG 236220
 TGTCAACTTG ACTGAGTCAG GGGATAACCA GCTATCTGGT TAAACATTAT TTCTGGCTGT 236280
 GTTTGTGAGC GTGTTTCTGG ATGAGATTAG CCTTTGAATA GGTGATCCTA GTAAAGTAAA 236340
 CTGTCTTTCC CAGTGTGGAT GGCATTATGC CACCTGATAT TCAGGGTCTG AATAGAAGAA 236400
 AAGGCAGAGG AAGGGGAAT TTGGGCCTTT TTTTCTGCCT CACTGCTTGA GCTGGGACAT 236460
 CTCATCTGGT CTCCTGCTCT TGAAGTGGGA TTTACATCAT CAGTTCCTCT GGTTCTCAGG 236520

CCTTCAGATT CAGACTGAAT CATACCACCA GCTTTCCTGG GTCTCCAGCT TGCAGATTAC 236580
 AGATCATGGG ACTCCTCATC TTCCATAAAT GCATGAGCCA ATTCAGTCTA TGTCCCTGAA 236640
 AACTGCCCCA CTGCAGATTA AGGCTTTTTT CCACTAGGTG AAATAAGAA GCTTGTTAGA 236700
 CAGATTTCCC TTCATCCAGT GCCCTCTCCT CTTTAAGTTA CAACACATTG GCTACACCTA 236760
 AGTGCAGGGG TGGGGATGAG GGTATAGTCC TCTTGTTTGC TGAGAAGAGA ACTGTATTGG 236820
 GAAAGCTCTA GAAGTGTTTG ATACATACAT AAACAAGGCA TGGTTTTTGC ACTTAATTTT 236880
 ACATTACATT TTTCCAGAA AAAAAGGAAT GTATAGGCAT CACGTAAGTG TACTAGCTGG 236940
 AGTCATTCTT CCTGATTATC AAAGGTAAAC AGTTATTAAT CCTATACCA GATGTCAAGG 237000
 AGAAGTACTT TTGGAACACA AGGAATTCTC TGGGAGTCCT TACTACTCTC AAGCCCAGTG 237060
 AAAAAGTTAA TGAAAACTA TAGTACCTTC CTATAAGCTG GATGACTAAT TACCAGGCTC 237120
 ATTTAGGAAT TTGCCTTACC AAGTAAAACA TAAGGGCAGC TGAGGTGCTG ACTGAAGACA 237180
 AATGGAGCAT AGAATAAGAG TAGTAAAGAA TGCCAAAAAT GCTGTCATGT ATCCATTGAC 237240
 AAAAGGAGCT ATAAAGCCTT TAGGTATTTT CACACTTGCT CTGTTACGTA AATGTATGTG 237300
 TGTGTGTGTG TGTGTGTGTG TGTGTG 237326

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGTTAGAACG CGGCTACAAT

20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCGATTCAT TAATGCAGGT 20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTAAAACG ACGGCCAGTC 20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCAGGAAACA GCTATGACC 19

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCATCAGCGA TTAATTCTA C 21

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTGCATTGTG GTGAAATCAG GG

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGAGTAATT GTTTAAGGTG C

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGAGTAATT GTTTAAGGTG T

21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGAAGAGATA GATATGGTGG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATGTGACC GTCCCATGAG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAACTGAATA TGCAGAAAAA AGTACACC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGTAGCTGGG ACTCACGGTG T

21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGTAGCTGGG ACTCACGGTG C

21

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGCCACCAC TCCCAGCTCA T

21

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCACACACCG ATTGG

15

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAAACTGAT CTTTGA

16

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TATATATATA TATA

14

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAAAAAAAAA AAAA

14

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGGATGGTCT

10

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTGTTGTTGT TG

12

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTTTTTTTTT TTTT

14

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AATAATAATA AT

12

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTTTTTTTT T

11

2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATATATATAT ATATATATAT

20